

SEQUENCE LISTING

<110> Barber, Elizabeth K

<120> Gene Expression Control Element DNA

<130> 896034605001

<150> US 60/237,079

<151> 2000-09-30

<160> 33

<170> PatentIn version 3.1

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<211> 137

<212> DNA

<213> human

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<221> exon

<222> (3) .. (137)

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<221> polyA\_site

<222> (130) .. (135)

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0996664-092891

0595664-09304  
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Tyr Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu  
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tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95  
Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys  
15 20 25

ggt aga aat agc atg aga agc cgt gtt tga tgt taa tta att 137  
Gly Arg Asn Ser Met Arg Ser Arg Val Cys Leu Ile  
30 35 40

<210> 2

<211> 996

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<222> (1) .. (996)

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<221> misc\_feature

<222> (710) .. (996)

<223> Nucleotides 710-996 are homologous to a portion of human dystroph  
in DNA in the region of exon 79 except that nucleotides 860-996 a  
re inverted in comparison to the orientation of the same sequence  
in the dystrophin DNA

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gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag 48  
Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu  
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taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96  
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro

20										25					30					
atc	atg	gaa	tat	tcc	tgt	tct	gat	aga	aat	ctt	gtg	ctt	atc	tat	gga	144				
Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val	Leu	Ile	Tyr	Gly					
				35					40					45						
att	ctt	ttg	ata	tat	att	tac	att	ggg	aac	ctg	aat	gta	gct	tga	cat	192				
Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu	Asn	Val	Ala		His					
			50					55					60							
ttt	tcc	atg	taa	aca	cca	gta	gcc	tga	tcc	aac	att	aag	ctg	ata	cta	240				
Phe	Ser	Met		Thr	Pro	Val	Ala		Ser	Asn	Ile	Lys	Leu	Ile	Leu					
				65						70					75					
aca	aac	aac	gtg	taa	tgg	ctt	cat	taa	taa	ggc	ttt	gct	tct	tcc	tgg	288				
Thr	Asn	Asn	Val		Trp	Leu	His			Gly	Phe	Ala	Ser	Ser	Trp					
					80							85								
aaa	ctg	gtg	aaa	aat	caa	acc	ttg	ttg	tgt	aca	ccc	tcg	atg	cag	ctt	336				
Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu					
	90					95					100									
ctg	tgt	tgt	ctt	cac	cca	gaa	atg	ggg	aat	gat	ttc	cca	aat	ggc	aaa	384				
Leu	Cys	Cys	Leu	His	Pro	Glu	Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys					
105					110					115					120					
gaa	aca	gag	tga	tgc	tat	cta	tct	gca	cct	ttt	gta	aag	tct	gtc	ttt	432				
Glu	Thr	Glu		Cys	Tyr	Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe					
					125					130					135					
ctt	tct	ctt	tgt	ttt	cca	gga	cac	aat	gta	gga	agt	ctt	ttc	cac	atg	480				
Leu	Ser	Leu	Cys	Phe	Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met					
				140					145					150						
gca	gat	gat	ttg	ggc	aga	gcg	atg	gag	tcc	tta	gta	tca	gtc	atg	aca	528				
Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr					
			155					160					165							
gat	gaa	gaa	gga	gca	gaa	taa	atg	ttt	tac	aac	tcc	tga	ttc	cag	cat	576				
Asp	Glu	Glu	Gly	Ala	Glu		Met	Phe	Tyr	Asn	Ser		Phe	Pro	His					
			170					175						180						
ggg	ttt	tat	aat	att	cat	aca	aca	aag	agg	att	aga	cag	taa	gag	ttt	624				
Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln		Glu	Phe					
			185					190						195						
aca	aga	aat	aaa	tct	ata	ttt	ttg	tga	agg	gta	gtg	gta	tta	tac	tgt	672				
Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu		Arg	Val	Val	Val	Leu	Tyr	Cys					
			200						205					210						
aga	ttt	cag	tag	ttt	cta	agt	ctg	tta	ttg	ttt	tgt	taa	caa	tgg	cag	720				
Arg	Phe	Gln		Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys		Gln	Trp	Gln					
				215					220					225						
gtt	tta	cac	gtc	tat	gca	att	gta	caa	aaa	agt	tat	aag	aaa	act	aca	768				
Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr					
				230					235					240						

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816  
 Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr  
 245 250 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864  
 His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr  
 260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912  
 Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr  
 275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960  
 Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg  
 285 290 295

aat agc atg aga agc cgt gtt tga tgt taa tta att 996  
 Asn Ser Met Arg Ser Arg Val Cys Leu Ile  
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<210> 3

<211> 13

<212> PRT

<213> human

<400> 3

Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn  
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<210> 4

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Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala Asp Thr Met  
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Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp  
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Glu Glu

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F03301-4929550

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gatgggatac atcttttcc

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<210> 24

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<400> 24

caagctacat tcaggttccc

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<210> 25

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Met Phe Val Asn Thr Thr Lys Val Glu Lys Met Tyr Pro Ile Met Glu  
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Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly Ile Leu Leu  
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Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys  
 35 40 45

Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln  
 50 55 60

Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe  
 65 70 75 80

Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg  
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Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser  
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Glu Val Glu Ile Ala  
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<223> Putative membrane-spanning segment

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20 25 30

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35 40 45

Gly Asn Leu Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala  
50 55 60

Arg Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His  
65 70 75 80

Lys Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu  
85 90 95

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met  
100 105 110

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0906264-092304

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr Leu Ser  
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Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe Pro Gly His  
130 135 140

Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu Gly Arg Ala Met  
145 150 155 160

Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu Gly Ala Glu Lys Met  
165 170 175

Phe Tyr Asn Ser Arg Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr  
180 185 190

Lys Arg Ile Arg Gln Lys Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu  
195 200 205

Arg Arg Val Val Val Leu Tyr Cys Arg Phe Gln Lys Phe Leu Ser Leu  
210 215 220

Leu Leu Phe Cys Lys Gln Trp Gln Val Leu His Val Tyr Ala Ile Val  
225 230 235 240

Gln Lys Ser Tyr Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys  
245 250 255

Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu  
260 265 270

Lys Gln Leu Lys Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn  
275 280 285

Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn  
290 295 300

Thr Pro Lys Pro Lys Arg Gly Arg Asn Ser Met Arg Ser Arg Val Arg  
305 310 315 320

Cys Lys Leu Ile

Descriptive statistics	
<i>N</i>	100
Age	20.5
Gender	50
SES	2.5
Cognitive ability	
<i>M</i>	100
<i>SD</i>	15
Range	70-130
Personality	
<i>M</i>	50
<i>SD</i>	10
Range	30-70
Stress	
<i>M</i>	50
<i>SD</i>	10
Range	30-70
Coping strategies	
<i>M</i>	50
<i>SD</i>	10
Range	30-70
Social support	
<i>M</i>	50
<i>SD</i>	10
Range	30-70
Health status	
<i>M</i>	50
<i>SD</i>	10
Range	30-70
Quality of life	
<i>M</i>	50
<i>SD</i>	10
Range	30-70
Correlation matrix	
Age	0.15
Gender	0.05
SES	0.20
Cognitive ability	0.30
Personality	0.25
Stress	0.20
Coping strategies	0.15
Social support	0.10
Health status	0.05
Quality of life	0.05

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1				5					10					15		
att	att	att	ttc	aac	cca	agt	aaa	agc	aga	gag	aaa	ata	gcc	acc	tcc	96
Ile	Ile	Ile	Phe	Asn	Pro	Ser	Lys	Ser	Arg	Glu	Lys	Ile	Ala	Thr	Ser	
			20					25					30			
acc	ata	gcc	tca	gaa	gca	agc	caa	cag	cct	gaa	aca	gct	ttg	aaa	tga	144
Thr	Ile	Ala	Ser	Glu	Ala	Ser	Gln	Gln	Pro	Glu	Thr	Ala	Leu	Lys		
		35					40					45				
aaa	gtt	ggg	gtg	gcg	gtg	atg	gtg	gca	gtg	ata	atg	gtg	acc	gat	ggg	192
Lys	Val	Gly	Val	Ala	Val	Met	Val	Ala	Val	Ile	Met	Val	Thr	Asp	Gly	
		50					55					60				
tgg	gtg	ctg	gtg	atg	gta	gtg	gta	gtt	gtg	aag	gtg	gtg	atg			234
Trp	Val	Leu	Val	Met	Val	Val	Val	Val	Val	Lys	Val	Val	Met			
	65					70				75						